RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _/o/766,752_

Source: _____

Date Processed by STIC: _____2/19/04~_____

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
       http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>, EFS Submission
   User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
   2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
   Box Sequence, Room 4B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED   SUGGESTED CORRECTION   SERIAL NUMBER: _10/766,752_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
     Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
     prevent "wrapping."

2 ____ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
     Numbering   use space characters, instead.

4 ____ Non-ASCII   The submitted file was **not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
ensure your subsequent submission is saved in ASCII text.**

5 ____ Variable Length   Sequence(s) ____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules,
each n or Xaa can only represent a single residue.** Please present the **maximum** number of each
residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
     "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
Artificial or Unknown sequences.**

7 ____ Skipped Sequences   Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
     (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
     (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
     (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
     This sequence is intentionally skipped

     Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
     (NEW RULES)   <210> sequence id number
     <400> sequence id number
     000

9 ____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
     (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
     In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
     Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
     is Artificial Sequence

11 ✓ Use of <220>   Sequence(s) _2-6_ missing the <220> "Feature" and associated numeric identifiers and responses.
     Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
     "Unknown." Please explain source of genetic material in <220> to <223> section.
     (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
     "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa   "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/766,752

DATE: 02/09/2004
TIME: 10:32:41

Input Set : A:\30331008008.txt
Output Set: N:\CRF4\02062004\J766752.raw

```
 4 <110> APPLICANT: Carney, Darrell H.
 6 <120> TITLE OF INVENTION: Use of Thrombin-Derived Peptides for the Therapy
 7       of Chronic Dermal Ulcers
 9 <130> FILE REFERENCE: 3033.1008-008
11 <140> CURRENT APPLICATION NUMBER: US/10/766,752
12 <141> CURRENT FILING DATE: 2004-01-27
14 <150> PRIOR APPLICATION NUMBER: PCT/US02/01151
15 <151> PRIOR FILING DATE: 2002-01-16
17 <150> PRIOR APPLICATION NUMBER: US 60/308,198
18 <151> PRIOR FILING DATE: 2001-07-27
20 <160> NUMBER OF SEQ ID NOS: 6
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 23
26 <212> TYPE: PRT
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: fragment of human thrombin
32 <400> SEQUENCE: 1
33 Ala Gly Tyr Lys Pro Asp Glu Gly Lys Arg Gly Asp Ala Cys Glu Gly
34  1               5                  10                  15
35 Asp Ser Gly Gly Pro Phe Val
36               20
39 <210> SEQ ID NO: 2
40 <211> LENGTH: 23
41 <212> TYPE: PRT
42 <213> ORGANISM: Artificial Sequence
44 <220> FEATURE:
45 <223> OTHER INFORMATION: Alanine at position 1 is optionally N-acylated.
47 <223> OTHER INFORMATION: Valine at position 23 is optionally C-amidated.
49 <221> NAME/KEY: VARIANT
50 <222> LOCATION: 15
51 <223> Xaa = Glu or Gln
53 <221> NAME/KEY: VARIANT
54 <222> LOCATION: (22)...(22)
55 <223> Xaa = Phe, Met, Leu, His or Val
58 <400> 2
59 Ala Gly Tyr Lys Pro Asp Glu Gly Lys Arg Gly Asp Ala Cys Xaa Gly
60  1               5                  10                  15
61 Asp Ser Gly Gly Pro Xaa Val
62               20
65 <210> SEQ ID NO: 3
66 <211> LENGTH: 33
```

Does Not Comply
Corrected Diskette Needed

pp 1-3

needs explanation in <2207-<2237 section.
(see item 11 on Error Summary Sheet)

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/766,752

DATE: 02/09/2004
TIME: 10:32:41

Input Set : A:\30331008008.txt
Output Set: N:\CRF4\02062004\J766752.raw

```
     67 <212> TYPE: PRT
     68 <213> ORGANISM: Artificial Sequence        see item 11 on Error Summary sheet
     70 <220> FEATURE:
     71 <223> OTHER INFORMATION: Asparatic acid at position 1 is optionally
     72       N-acylated.
     74 <223> OTHER INFORMATION: Phenylalanine at position 33 is optionally
     75       C-amidated.
W--> 77 <400> 3
     78 Asp Asn Met Phe Cys Ala Gly Tyr Lys Pro Asp Glu Gly Lys Arg Gly
     79 1               5                   10                  15
     80 Asp Ala Cys Glu Gly Asp Ser Gly Gly Pro Phe Val Met Lys Ser Pro
     81          20                  25                  30
     82 Phe

     86 <210> SEQ ID NO: 4
     87 <211> LENGTH: 33
     88 <212> TYPE: PRT
     89 <213> ORGANISM: Artificial Sequence        same error
     91 <220> FEATURE:
     92 <223> OTHER INFORMATION: Asparatic acid at position 1 is optionally
     93       N-acylated.
     95 <223> OTHER INFORMATION: Phenylalanine at position 33 is optionally
     96       C-amidated.
W--> 98 <221> NAME/KEY: VARIANT
W--> 99 <222> LOCATION: (20)...(20)
W--> 100 <223> Xaa = Glu or Gln
W--> 102 <221> NAME/KEY: VARIANT
W--> 103 <222> LOCATION: (27)...(27)
W--> 104 <223> Xaa = Phe, Met, Leu, His or val
W--> 106 <400> 4
     107 Asp Asn Met Phe Cys Ala Gly Tyr Lys Pro Asp Glu Gly Lys Arg Gly
     108 1               5                   10                  15
W--> 109 Asp Ala Cys Xaa Gly Asp Ser Gly Gly Pro Xaa Val Met Lys Ser Pro
     110          20                  25                  30
     111 Phe

     115 <210> SEQ ID NO: 5
     116 <211> LENGTH: 23
     117 <212> TYPE: PRT
     118 <213> ORGANISM: Artificial Sequence        same
     120 <220> FEATURE:
     121 <223> OTHER INFORMATION: Alanine at position 1 is optionally N-acylated.
     123 <223> OTHER INFORMATION: Valine at position 23 is optionally C-amidated.
W--> 128 <400> 5
     129 Ala Gly Tyr Lys Pro Asp Glu Gly Lys Arg Gly Asp Ala Cys Glu Gly
     130 1               5                   10                  15
     131 Asp Ser Gly Gly Pro Phe Val
     132          20

     135 <210> SEQ ID NO: 6
     136 <211> LENGTH: 23
     137 <212> TYPE: PRT
```

```
138 <213> ORGANISM: Artificial Sequence        same
140 <220> FEATURE:
141 <223> OTHER INFORMATION: Valine at position 23 is amidated with -NH2.
143 <400> SEQUENCE: 6
144 Ala Gly Tyr Lys Pro Asp Glu Gly Lys Arg Gly Asp Ala Cys Glu Gly
145 1               5                   10                  15
146 Asp Ser Gly Gly Pro Phe Val
147             20
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 02/09/2004
PATENT APPLICATION: US/10/766,752   TIME: 10:32:42

Input Set : A:\30331008008.txt
Output Set: N:\CRF4\02062004\J766752.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos. 15,22
Seq#:4; Xaa Pos. 20,27

```
                    VERIFICATION SUMMARY          DATE: 02/09/2004
                    PATENT APPLICATION:  US/10/766,752    TIME: 10:32:42

                    Input Set : A:\30331008008.txt
                    Output Set: N:\CRF4\02062004\J766752.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:49 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:50 M:281 W: Numeric Fields not Ordered, <222> Sort in ascending order!
L:51 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:53 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:54 M:281 W: Numeric Fields not Ordered, <222> Sort in ascending order!
L:55 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:58 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:59 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
M:341 Repeated in SeqNo=2
L:77 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:98 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:99 M:281 W: Numeric Fields not Ordered, <222> Sort in ascending order!
L:100 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:102 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:103 M:281 W: Numeric Fields not Ordered, <222> Sort in ascending order!
L:104 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:106 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:16
L:128 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
```